

H<sup>2</sup>  
nucleotide sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 2207 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein said primer contains at least 5 and no more than 30 nucleotides.

SUB I  
H<sup>3</sup>  
10. (Four Times Amended) The primer according to claim 8, wherein said primer consists essentially of a nucleotide sequence selected from the group consisting of SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10 and SEQ ID NO:12.

SUB I  
H<sup>4</sup>  
17. (Three Times Amended) The reagent according to claim 11, further comprising at least one primer consisting essentially of a segment of at least five contiguous nucleotides of a nucleic acid that is identical or fully complementary to a first sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence.

SUB I  
H<sup>5</sup>  
20. (Three Times Amended) The method according to claim 18, wherein before said DNA is exposed to said probe, said DNA is amplified in the presence of an enzymatic system with at least one primer, wherein said primer consists essentially of a segment of at least five contiguous nucleotides of a nucleic acid sequence that is identical or fully complementary to a sequence identified in SEQ ID NO: 1 or the corresponding RNA sequence.

SUB I  
H<sup>6</sup>  
21. (Three Times Amended) A synthetic or isolated nucleic acid fragment that consists essentially of a nucleotide sequence having at least 85% homology with a reference sequence that is identical or fully complementary to a sequence starting at nucleotide 1232 and ending at nucleotide 1825 of SEQ ID NO: 1 or the corresponding RNA sequence, wherein each segment of 30 contiguous nucleotides of said nucleotide sequence has at least 85% homology with a segment of 30 contiguous nucleotides of said reference sequence.

H<sup>7</sup>  
SUB I  
23. (Three Times Amended) A synthetic or isolated nucleic acid fragment that consists essentially of a nucleotide sequence having at least 85% homology with a reference